(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression. and further comprising:

(d)   generating a file containing information for display relating to a peak in the molecular topology, and

(e)   linking the information for display to the related peak in the molecular topography.

3.   (Amended)   A method in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second val e for a second polynucleotide-characteristic different from said first

characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide:

(b)   calculating for each polynucleotide from the first and second values a position,

and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the

polynucleotide in the display, the resulting display representing thereby a molecular topography

of gene expression,

wherein: (i) the first characteristic is a sequence identifier, and (ii) the second

characteristic is a measure of size.

5.   (Amended)   The method of Claim 2, wherein the polynucleotides are cDNAs or

fragments thereof.

6.   (Amended)   A method in a computer system for analyzing an displaying data on gene

expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating

polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide-characteristic different from said first

characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide:

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

wherein the polynucleotides are cDNAs or fragments thereof, and

wherein the polynucleotides are 3'-end fragments of restriction enzyme cleaved cDNAs.

11.   (Amended)   A method in a computer system for displaying differences in gene expression, comprising:

(1)   for each of two gene expression profiles to be compared generating a molecular topography according to a method in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression.

(2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;

(3) for each position, generating a peak for display from the difference; and

(4) displaying the respective difference peak at each of the positions in the two co-ordinate space.

12. (Amended) A method in a computer system for displaying differences in gene expression, comprising:

(1) for each of two gene expression profiles to be compared generating a molecular topography according to a method, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression.

(2)   for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;

(3)   for each position, generating a peak for display from the difference; and

(4)   displaying the respective difference peak at each of the positions in the two co-ordinate space,

wherein differences are displayed only if they meet or exceed a threshold value.

23.   (Twice amended)   A method in a computer system for displaying a series of in gene expression profiles in a molecular movie, comprising:

(1)   generating a plurality of molecular topographies according to a method, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression, and

(2)   displaying the molecular topographies in succession,

wherein the molecular topographies are delta plots.

24.   (Amended)   A computer program product, usable in a computer system, for analyzing and displaying gene expression in a molecular topography, the computer program product comprising:

a first program code that generates a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide- characteristic different from said first characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide; a second program code that calculates for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

a third program code that displays the peak for each polynucleotide at the calculated position for the polynucleotide in a display, the resulting display resulting thereby a molecular topography of gene expression, and further comprising

(d)   a fourth program code for generating a file containing information for display relating to a peak in the molecular topology, and